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gb_ba1:AF009912
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gb_ba1:AF009913
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Query length:
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- Q-/cgn1_1/USPTO_spool/US09494297/runat_06062001_115734_12308/app_query.fasta_1.825
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- FGAPEXT=7.000 - YGAPDP-10.000 - YGAPEXT=0.500 - DELOP-6.000
- DELEXT=7.000 - START-1 - MATRIX-SLOSED-pct - THR.MS-human40.cdi
- LIST=45 - DOCALIGN-200 - THR.SCORE-pct - THR.MSX-100 - THR.MIN-0
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Search time (sec): 2987.740000
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7 i X9995 S.equi fiz gene. 1/1997
44 AR083961 Sequence 2 from paten
6 i AF083960 Sequence 1 from paten
6 i AF083131 Moraxella catarrhalis
17 i AX067453 Sequence 28 from paten
8 i AF043133 Moraxella catarrhalis
20 i U31980 Streptococcus pyogenes
850 i AF00992 Thermoplasma volcan
20 i AF120104 Lactobacillus reuten
20 i AF120104 Lactobacillus reuten
30 i U4468 Lactococcus lactis sex
460 i AL13940 Homo sapiens Ghron
0 i D44498 Bacillus subtilis hspN
1 AF134726 Homo sapiens BAC cl
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AF009917 Streptococcus pyogenes
AF009917 Streptococcus pyogenes
AF009918 Streptococcus pyogenes
AF009918 Streptococcus pyogenes
AF009918 Streptococcus pyogenes
AF009919 Streptococcus pyogenes
                                                                                          | AF188483 Photorhabdus luminesc
| 1 AP000503 Homo sapiens genomi
| 1 Z23277 C.difficile gene for to
| 1 AC005505 Plasmodium falcipar
| 2 | 1 AC005139 Plasmodium falcipar
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AJ005646 Staphylococcus aureus AR067712 Sequence 8 from pater M81736 Staphylococcus aureus
                                           AR071281 Sequence 1 from pater
AF071083 Streptococcus pyogene
M59828 Human MHC class III HSF
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U31115 Group G streptococcus
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AUTHORS
TITLE
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ORGANISM
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MolesMicrobible 31 (1999) In press
2 (bases 1 to 10826)
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Cpa (cpa), and Nra (nra) genes compartial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (19-FEB-1996) RWTH Aachen, Institute of Medical Microbiology, Pauwelsstrasse 30, Aachen, Nrw, Federal Republic of Germany, 52074
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Podbielski A. Wolschnik, M.,
Characterization of nra, a g
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                                                                                                                                                                                          complement(1394.
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- 147.00
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! AE002147 Ureaplasma urealy
! AE002147 Ureaplasma urealy
! Al8434 Hybrid DNA molecule
! Al8436 assembled sequence f
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-10_signal
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complement(6161.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAEEQSVPNRQSSIQDYPWYGYDSYPKGYPDYSPLKTYHNLKVNLEGSKDYQAYCFNL
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SVAMSGSLFLDTRNHNDFTDDYSLIYGHHMAGNAMFGEIPKFLKKNFFNKHNKAIIET
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ATLKDGEQSSTYELGKDHKTDKSADEIVYTNKRDTQVFTGVGTLAPFAVLSIVAIGG
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KGKISTLLRVRGI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(3191. .3712)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(3191. .3712)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KFVAFSTCENFSTDNRVIVVGTIQE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KERKKLTVTIFACLKTDAFDQLVFNPNAITNQDQQRQLVDYISKRSKQFKPVKLKHHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VIYITKRKKAQVISQRMMMTIVQVINKAIDTLILIFCLVVLFLAGFGLWDSYHLYQQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'gene="cpa"
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                                                                                                                                                                                                                                                  'gene="nra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transl_table=11
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                                                                                   note-"promoter
                                                                                                                                                                                                                                                                                                         note="promoter 2"
                                                                                                                                                                                                                                                                                                                                                                                                                       'gene≖"cpa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon_start=1
                                                                                                                                                                                                                     note="extended promoter 2"
                                                            . 6325
                                                                                                                                                                                                 .7898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TepA"
                                                                                                                                                                                                                                                                                                                                                             promoter 2"
. .6166)
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Sg gene CDS

gene

CDS

Align seg 1/1

to reverse of: SPU49397

from: 1

to: 10826

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alignment_scores:
Quality:
                              alignment_block:
US-09-494-297-2 x SPU49397/rev
                                                                                 Ratio: 3.412
Percent Similarity: 4.784155
                                                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                                     gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -10_signal
                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                          1965.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8006. .8016
/note="ORF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QTGLTAVQLKYYCKELDDFFGNNLDITIKKGKIICCFVKPVKEFYLHQLYDTSTILKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EVLVGPFMGNGHFVTIIDYGTGNPYTSTTPLITGEIGEDFAYYLTESEQTPSAIGLNV
LLDENDKVKVAGGFMVQVLPEASEEEIARYEKRLQEMPAISHLLASKNHVDALLEAIY
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KRHQFAVSIPQTRIFRQLKKLFIYDCLTRSSRQVIENAFSLTFSQGDLDYLFLIYITT
                                                                                                                                                                                                                                                                                     complement (10782.
                                                                                                                                                                                                                                                                                                                                            10598. 10681
/note="putative transcription
                                                                                                                                                                                                                                                                                                                                                                                                     HQVHGEYPTWYEDYKVSPKMKIDGNSLDFVQNPQDLATVLKMIDTKLKELHLL"
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FMIEEIGVDAVMIGRAAMNNPYLFTQINHFFETGQELPDLPFAKKLDIAKDHLKRLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DINMGCPVNKVVKNEAGAKWLRDPDKIYHIVKEVTSVLDIPLTVKMRTGWADSSLAVE
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/note="ORF 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GDEPYKRLSEEPLSFQCDCSRERFEAALMTLPKADLQAMIDEDKGAEIVCQFCGTKLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KPDLVITHSRLIPFVKNDLVKGVTVAEFSFDKPDYSIASIQNLIYQLKDKKYQDFLNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FLFNLQHFYIEIPSFSLPTYTGNSNLYKALKNIVNQWLAQLPGKRHLNEKHLQLFCSH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NNSFASLQWTPQHIETCCHIFEKNDTFRLLLEPILKRLPQLNHSKQDLIKALMYFSKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAC97147.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="negative regulator of group A Streptococc1"
/codon_start=1
                                                                                                                                                                                                                                                                                                                    /rpt_type-inverted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="similar to Lactobacillus acidophilus dA/dG-kinase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /MEMISEKGLLYNNEKTLHMLHIDENEHPMSIQLFGGDAEGLKRAADFIQTNTKADIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'product-"unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="ORF 5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 8857
                                                                                 Length: 737
Gaps: 13
Percent Identity: 54.410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similar to Azospirillum brasilense nifR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        extended -10 signal"
                                                                                                                                                                                                                               .>10826)
                                                                                                                                                                                                                                                                                        .>10826)
                                                                                                                                                                                                                                                                                                                                                  terminator"
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شو	301	284 5139	268 5183	251 5215	234 5265	218 5315	201 5365	184 5409	168 5459	151 5509	134 5559	118 5609	101 5659	84 5709	68 5759	51 5803	34 5853	20 5903
sn $ValAsnSerPheGlnAlaArgValPheSerSerAsnAspIleGlyGl3$	SLeuLeuGluGlyAlaThTLeuGlnLeuThTGlyAsp 3 	OPTOASNG1nPrOG1nThrThrSerValLeuIleArgLysTyralaileG 3 :: :: :: 	rLysProProThrProGlyAspProProMetPr 2 ::: racTcccccaaaaccaggagagagagcc 5	AspLysTyr	rLysMetProLysGlnValProAspAspPheGlnLeuSerIlePheGluS 2	SerLeuMetArgGlnAlaLeuLysGlnLeuIleAspProAsnLeuAlaTh 2 ::: :::	GluSerGluSerAsnLeuValSerT ::::: GAAGCTCGAAGTAATGGTATTAATG	nGluAlaValTrpTyrTyr5erAspAsnAlaProIleSerAsnProAspG 2 ::: ::: :::	AsnGlyIleMetGluGlyLeuGluProLeuAsnAlaIleArgValThrGl 1 	euAsnGlnLysLeuArgAlaValMetTyrAsnGlyHisProGlnAsnAla 1 -:: -::: TACAACAAATATATTGAGGATTCTCTATAATGGATATCCTAATAATCGT 5	YrAlaMetSerProArgIleThr ::: TAGCAGATAAACCAAGAATAGAA	GlySeraspSerSerValLysLysTrpTyrLysLysHisAspGlyIleSe 1 	erArgSerTyrGlnValTyrCysPheAsnLeuLysLysAlaPheProLeu 1 :::::: :::	TTyrLysGlnPheArgValAlaHisAspLeuArgValAsnLeuGluGlyS 1	YTValA - ATCCTA	. +	eLeumetllePheAlaLeuValThrSerMetValGlyAlaLySThrValP 5 ::: :::	.PheThrValThrLeuValG ::: AACGACGATCGGATTACTGA
	17 043	090	84 140	67 184	51 216	34 266	17 316	01 366	84 410	67 460	51 510	34	17 610	01	710	760	804	854
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4149 626	TAAAAAGCAAGAAGTTATTCCAGTAACTCACAGTTTGACAGTGAAA hrValThrGlyLeuAlaGlyAspArgThrLysAspPheHisPheGl	4198 610
09	luAspLysLysGluValIleProValThrHisAsnLeuThrLeuArg	59
594 4199	ulleGlyThrGlnTrpHisProGluAspLeuValAspIleIleArgMetG	577 4248
577 4249	LeuThraspLeuAspPhePheIleProAsnAsnLysTyrGlnSerLe	561 4298
560 4299	laValAlaLysIleLeuValGluTyrAlaGlnAspSerAsnProProGln	544 4348
544 4349	LysaspTyrH1sGlyPheGlyAspMetAsnAspSerThrLeuA 	530 4398
529 4399	IleTyrTyrPheThrAspSerAlaGluLeuAspLysAspLysLeu	515 4448
514 4449	luTyrSerGlyLeuThrGluThrGlnLeuArgi ::: ::: 	498 4496
498 4497	SI1eLysLysValI1eGluLysGlyTyrArgGluLysGlyGlnAlar1eG	481 4542
481 4543	LysTyrThrValLysProArgAspThrAspProAspThrPheLeuLysH1	465 4592
464 4593	hrThrGlyGluValLysTyrThrHisTleAlaGlyArgAspLeuPhe:: 	449 4642
449 4643	SSETPTOPTOASpSETGluAspGlyGlyLysThIMEtThTPTOASpPheT	432 4692
432 4693	ASDLYSASDG1YSerSerG1DValValTyrCysPheAsDAlaAspLeuLY	416 4742
415 4743) heServalLeuThrThrGlnAsnTyrAlaLysPheTyrTyrAlaLys ::: ::: AAGAAGTACTCTCGGGTTTTACTCCATACGGAAAATTCTATTACGCTACA	400 4792
400 4793	SGluIleValGluProTyrSerValGluAlaTyrAsnAspPheGluGluP ::::::	383 4842
383 4843	LysValTyrThrIle	368 4892
367 4893	roAlaGlyTyrSerIleAlaGluProIleThrPheLysValGluAlaGly	351 4942
351 4943	uArgIleGluLeuSerAspGlyThrTyrThrLeuThrGluLeuAsnSerP 	334 4992
4993	GAAGGAAGTGGTTTTCAAGAAAAAGACTTTCAAAGTAATAGTTTAGGAGA	5042

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REFERENCE
AUTHORS
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LOCUS STRPRINF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: gb_ba3:STRPRTNF
                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3798 AACAGATGGGGCTATCTATCTTTGGTTGTTATTACTTGTTCCACTTGGGT 3749
                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4148 AAAACAGTAGTCGGTGAGTTGGGAGATAAAACTAAAGGCTTCCAATTTGA 4099~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                643 hraspLysThrasnLeuGluPheLysaspGlyLysalaThrIleasnLeu 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     626 ulleGluLeuLysAsnAsnLysGlnGluLeuLeuSerGlnThrValLysT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         euGlyIleTrp 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ThrLeuAlaPheGluAsnAsnLysGluProValValProThrGlyValAs 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TATTGGTTTGG 3738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pGlnLysIleAsnGlyTyrLeuAlaLeuIleValIleAlaGlyIleSerL 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAAGTCACTTTTGAAAACCGAAAAGATCTTGTCCCACCAACTGGTTTGAC 3799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAGTTAGTCAAGAAGCGCAGTCAGTAGGGTAAGGATATAACAGAAGACAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TACTCTGAAAGAGGCTGAAGCTAAGGATTATATAGTAACCGTTGATAACA 3899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rLeuValLysGluThrAspSerGluGlyTyrLysValLysValAsnSerG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGCATGGTGACACCATAAGAATAGAAGGATTACCGACGGGATATTCTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LysHisClyGluSerLeuThrLeuGlnGlyLeuProGluGlyTyrSerTy 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTTGAGTTGAAAGATAAAACTGGACAGCCTATTGTTAACACTCTAAAAA 4049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lnGluValAlaAsnAlaThrValSerLysThrGlyIleThrSerAspGlu 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           adhesin; fibronectin-binding protein; Streptococcus pyogenes (strain JRS75) Streptococcus pyogenes
Bacteria; Firmicutes; Bacillus/Clostri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sela,S., Aviv,A., Burstien,I., Tovi,A., Caparon,M.G. and Hanski,E. Protein F: An adhesin of Streptococcus pyogenes binds fibronectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus.

1 (bases 1 to 2845)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus pyogenes fibronectin-binding protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                two distinct domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Microbiol. 10, 1049-1055 (1993)
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                                                                                                                                                                                                                                             /gene="prtF"
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                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                         'function="binds fibronectin"
                                                                                                                                                                                                    /codon_start=1
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                                                                                                                                                                                                                                                                                         'gene≖
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ORIGIN
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KEYWORDS SOURCE

ACCESSION

3898

710

3948

676

3998

4048

660

VERSION

FEATURES

gene CDS

TITLE

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US-09-494-297-2 x STRPRTNF
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688 TATTTGGACTCGTTATCATGACTTGAGAGTAAATTTAAATGGGAGTCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  594 CCGATGAGAAGACTGTGCCGAGTCATAGTAGTCCA.....AATCCTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           544 GCTTTTGGCATGCGGGGTGCTATCGGTTTTGGTCAAGTAGCCTATGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    494 ACAAAAAGAAAAAGGCGATTTGCTGTCACTTTAGTGGGAGTCTTTTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36\ {	t tilePheAlaLeuValThrSerMetValGlyAlaLysThrValPheGlyL}
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                                                     AGTTTGGCATTACTCAGATAATTCACAATATCAATTT...GAGACATTAT 1034
                                                                                                                               TATATGAAAGGACTGGAGCATTTAAATGCTATTACTGTAACACAATATGC
                                                                                                                                                                                                                                                                                 CTTTGTAGATTATGCTCACACTACTAAACTAGGTAAAGAAGAGTTGGAGC
                                                                                          aValTrpTyrTyrSerAspAsnAlaProIleSerAsnProAspGluSerP
                                                                                                                                                                   IleMetGluGlyLeuGluProLeuAsnAlaIleArgValThrGlnGluAl
                                                                                                                                                                                                        AGAGGCTCTTAAGTTTACTGTATAATGCGTATCCCAACGATGCTAATGGT
                                                                                                                                                                                                                                           lnLysLeuArgAlaValMetTyrAsnGlyHisProGlnAsnAlaAsnGly
                                                                                                                                                                                                                                                                                                                      {\tt sPheGluAspTyrAlaMetSerProArgIleThrGlyAspGluLeuAsnG}
                                                                                                                                                                                                                                                                                                                                                                                   AspSerSerValLysLysTrpTyrLysLysHisAspGlyIleSerThrLy 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                            erTyrGlnValTyrCysPheAsnLeuLysLysAlaPheProLeuGlySer 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     euValGluSerSerThrProAsnAlaIleAsnProAspSerSerSerGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTACCAAGTTTATTGTTTTAATATTCAATCTAATTATCCTAGCCAAAAA
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1631. 2170
/gene="prtF"
/note="repeat domain 2
a 472 c 616 g
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LDGQEVPEKPSIDLPIEVPKYEFINNKDQSPLAGESGETEYITEVYGNQQNPVDLDKKL
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LMGGQSESVEFTKDTQTGMSGQTPQLETEDYKEPEVLMGGQSESVEFTKDTQTGGMSG
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QTTPQVETEDTKEPEVLMGGQSESVEFTKDTQTGMSG
QTSQVEFTKDTQTGMSGFSETATVVEDTRPKLVFHFDNNEPKVEENREKPTKNITPILP
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